



SEQUENCE LISTING

<110> Cancer Research Campaign Technology Limited
Durrant, Linda G
Spendlove, Ian

<120> Tumour Associated Antigen 791Tgp72

<130> SJK/BP5758875

<140> 09/523,035

<141> 2000-10-12

<150> PCT/GB99/00582

<151> 1999-02-26

<150> GB 9804065.2

<151> 1998-02-26

<160> 13

<170> PatentIn Ver. 2.1

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<211> 2102

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)..(1211)

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Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala Leu Pro Leu Leu

1

5

10

15

ggg gag ctg ccc cgg ctg ctg ctg ctg gtg ctg ttg tgc ctg ccg gcc 158
 Gly Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala
 20 25 30

gtg tgg ggt gac tgt ggc ctt ccc cca gat gta cct aat gcc cag cca 206
 Val Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro
 35 40 45

gct ttg gaa ggc cgt aca agt ttt ccc gag gat act gta ata acg tac 254
 Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr
 50 55 60

aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag aag gac tca gtg 302
 Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val
 65 70 75

atc tgc ctt aag ggc agt caa tgg tca gat att gaa gag ttc tgc aat 350
 Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn
 80 85 90 95

B1
 cgt agc tgc gag gtg cca aca agg cta aat tct gca tcc ctc aaa cag 398
 Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln
 100 105 110

cct tat atc act cag aat tat ttt cca gtc ggt act gtt gtg gaa tat 446
 Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr
 115 120 125

gag tgc cgt cca ggt tac aga aga gaa cct tct cta tca cca aaa cta 494
 Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu
 130 135 140

act tgc ctt cag aat tta aaa tgg tcc aca gca gtc gaa ttt tgt aaa 542
 Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys
 145 150 155

aag aaa tca tgc cct aat ccg gga gaa ata cga aat ggt cag att gat 590
 Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp
 160 165 170 175

gta cca ggt ggc ata tta ttt ggt gca acc atc tcc ttc tca tgt aac 638
 Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn
 180 185 190

aca ggg tac aaa tta ttt ggc tcg act tct agt ttt tgt ctt att tca 686
 Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser
 195 200 205

ggc agc tct gtc cag tgg agt gac ccg ttg cca gag tgc aga gaa att 734
 Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile
 210 215 220

tat tgt cca gca cca cca caa att gac aat gga ata att caa ggg gaa 782
 Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu
 225 230 235

B1
 cgf gac cat tat gga tat aga cag tct gta acg tat gca tgt aat aaa 830
 Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys
 240 245 250 255

gga ttc acc atg att gga gag cac tct att tat tgt act gtg aat aat 878
 Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn
 260 265 270

gat gaa gga gag tgg agt ggc cca cca cct gaa tgc aga gga aaa tct 926
 Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser
 275 280 285

cta act tcc aag gtc cca cca aca gtt cag aaa cct acc aca gta aat 974
 Leu Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn
 290 295 300

gtt cca act aca gaa gtc tca cca act tct cag aaa acc acc aca aaa 1022
 Val Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys
 305 310 315

acc acc aca cca aat gct caa gca aca cgg agt aca cct gtt tcc agg 1070
 Thr Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg
 320 325 330 335

aca acc aag cat ttt cat gaa aca acc cca aat aaa gga agt gga acc 1118
 Thr Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr
 340 345 350

act tca ggt act acc cgt ctt cta tct ggg cac acg tgt ttc acg ttg 1166
 Thr Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu
 355 360 365

aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg ctg act tag 1211
 Thr Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu Leu Thr
 370 375 380

ccaaagaaga gttaagaaga aaatacacac aagtatacag actgttccta gtttcttaga 1271

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gtctttaaga tgtgtagga atgtcaacag agcaaggaga aaaaaggcag tcctggaatc 1391

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cctttcctaa aagtgaaga aagcatagag atttggtcgt atttagaatg ggatcacgag 1511

gaaaagagaa ggaaagtgat tttttccac aagatctgta atgttatttc cacttataaa 1571

ggaaataaaa aatgaaaaac attatttgga tatcaaaagc aaataaaaaac ccaattcagt 1631

ctcttctaag caaaattgct aaagagagat gaaccacatt ataaagtaat ctttggtgt 1691

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aaccaggggt gttgatggtg ataagggagg aatatagaat gaaagactga atcttccttt 1811

gttgcaaaa tagagtttg aaaaagcctg tgaaaggtgt cttctttgac ttaatgtctt 1871

B1
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taaaagtatc cagagatact acaatattaa cataagaaaa gattatatat tattttctgaa 1931
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 tttatgacag tgaacattct gattttacat gtaaaacaag aaaagttgaa gaagatatgt 2051
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<211> 381

<212> PRT

<213> Homo sapiens

<400> 15

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10

15

Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu Cys Leu Pro Ala Val

20

25

30

Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro Asn Ala Gln Pro Ala

35

40

45

Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val Ile Thr Tyr Lys

50

55

60

Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys Asp Ser Val Ile

65

70

75

80

Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu Phe Cys Asn Arg

85

90

95

B1
WK

Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser Leu Lys Gln Pro
 100 105 110

Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val Val Glu Tyr Glu
 115 120 125

Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser Pro Lys Leu Thr
 130 135 140

Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu Phe Cys Lys Lys
 145 150 155 160

Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly Gln Ile Asp Val
 165 170 175

Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe Ser Cys Asn Thr
 180 185 190

Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys Leu Ile Ser Gly
 195 200 205

B₂V Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys Arg Glu Ile Tyr
 210 215 220

Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile Gln Gly Glu Arg
 225 230 235 240

Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala Cys Asn Lys Gly
 245 250 255

Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr Val Asn Asn Asp
 260 265 270

Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg Gly Lys Ser Leu
 275 280 285

Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro Thr Thr Val Asn Val
 290 295 300

Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys Thr Thr Thr Lys Thr
 305 310 315 320

Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr Pro Val Ser Arg Thr
 325 330 335

Thr Lys His Phe His Glu Thr Thr Pro Asn Lys Gly Ser Gly Thr Thr
 340 345 350

Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr Cys Phe Thr Leu Thr
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 370 375 380

<210> 3

<211> 586

<212> DNA

<213> Homo sapiens

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agttctgcaa tcgtagctgc gaggtgccaa caaggctaaa ttctgcatcc ctcaaacagc 180

cttatatcac tcagaattat tttccagtcg gtactgttgt ggaatatgag tgccgtccag 240

gttacagaag agaaccttct ctatcaccaa aactaacttg cttcagaat ttaaaatggt 300

ccacagcagt cgaattttgt aaaaagaaat catgccctaa tccgggagaa atacgaaatg 360

gtcagattga tgtaccaggt ggcattat ttgatgcaac catctccttc tcatgtaaca 420

caggggtaca aattatttgg ctgacttct agtttttgtc ttatttcagg cagctctgtc 480

cagtggagtg acccgttgcc agaatgcaga gaaatttatg tccagcacca ccacaaattg 540

acatggaata atccagggga acgttgacca ttatggatat aaacgt 586

B1
w/

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 <212> DNA
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 <223> n is a or g or c or t

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 gcagagaaat ttattgtcca gcaccaccac aaattgacaa tggaataatt caaggggaac 180
 gtgaccatta tggatataga cagtctgtaa cgtatgcatg taataaagga ttcaccatga 240
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 cacctgaatg cagaggaaaa tctctaactt ccaaggctcc accaacagtt cagaaaccta 360
 ccacagtaaa tgttccaact acagaagtct caccaacttc tcagaaaacc accacaaaaa 420
 ccaccacacc aaatgctcaa gcaacacgga gtacacctgt ttccaggaca accaagcatt 480
 ttcatgaaac aaccccaaat aaaggaagtg gaaccacttc aggtactacc cgtcttctat 540
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 atatctgcag aattcgatgg gcgtagctgc gactcggcgg agtcccggcg gcgcgtcctt 180
 gttctaaccg ggccgcgc atg acc gtc gcg cgg ccg agc gtg ccc gcg gcg 231
 Met Thr Val Ala Arg Pro Ser Val Pro Ala Ala
 1 5 10
 ctg ccc ctc ctc ggg gag ctg ccc cgg ctg ctg ctg ctg gtg ctg ttg 279
 Leu Pro Leu Leu Gly Glu Leu Pro Arg Leu Leu Leu Leu Val Leu Leu
 15 20 25
 tgc ctg ccg gcc gtg tgg ggt gac tgt ggc ctt ccc cca gat gta cct 327
 Cys Leu Pro Ala Val Trp Gly Asp Cys Gly Leu Pro Pro Asp Val Pro
 30 35 40
 aat gcc cag cca gct ttg gaa ggc cgt aca agt ttt ccc gag gat act 375
 Asn Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr
 45 50 55
 gta ata acg tac aaa tgt gaa gaa agc ttt gtg aaa att cct ggc gag 423
 Val Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu
 60 65 70 75

B1

aag gac tca gtg atc tgc ctt aag ggc agt caa tgg tca gat att gaa 471
 Lys Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu
 80 85 90

gag ttc tgc aat cgt agc tgc gag gtg cca aca agg cta aat tct gca 519
 Glu Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala
 95 100 105

tcc ctc aaa cag cct tat atc act cag aat tat ttt cca gtc ggt act 567
 Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr
 110 115 120

gtt gtg gaa tat gag tgc cgt cca ggt tac aga aga gaa cct tct cta 615
 Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu
 125 130 135

tca cca aaa cta act tgc ctt cag aat tta aaa tgg tcc aca gca gtc 663
 Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val
 140 145 150 155

B1
 gaa ttt tgt aaa aag aaa tca tgc cct aat ccg gga gaa ata cga aat 711
 Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn
 160 165 170

ggc cag att gat gta cca ggt ggc ata tta ttt ggt gca acc atc tcc 759
 Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser
 175 180 185

ttc tca tgt aac aca ggg tac aaa tta ttt ggc tcg act tct agt ttt 807
 Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe
 190 195 200

tgt ctt att tca ggc agc tct gtc cag tgg agt gac ccg ttg cca gag 855
 Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu
 205 210 215

tgc aga gaa att tat tgt cca gca cca cca caa att gac aat gga ata 903
 Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile
 220 225 230 235

att caa ggg gaa cgt gac cat tat gga tat aga cag tct gta acg tat 951
 Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr
 240 245 250

gca tgt aat aaa gga ttc acc atg att gga gag cac tct att tat tgt 999
 Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys
 255 260 265

act gtg aat aat gat gaa gga gag tgg agt ggc cca cca cct gaa tgc 1047
 Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys
 270 275 280

aga gga aaa tct cta act tcc aag gtc cca cca aca gtt cag aaa cct 1095
 Arg Gly Lys Ser Leu Thr Ser Lys Val Pro Pro Thr Val Gln Lys Pro
 285 290 295

acc aca gta aat gtt cca act aca gaa gtc tca cca act tct cag aaa 1143
 Thr Thr Val Asn Val Pro Thr Thr Glu Val Ser Pro Thr Ser Gln Lys
 300 305 310 315

acc acc aca aaa acc acc aca cca aat gct caa gca aca cgg agt aca 1191
 Thr Thr Thr Lys Thr Thr Thr Pro Asn Ala Gln Ala Thr Arg Ser Thr
 320 325 330

cct gtt tcc agg aca acc aag cat ttt cat gaa aca acc cca aat aaa 1239
 Pro Val Ser Arg Thr Thr Lys His Phe His Glu Thr Thr Pro Asn Lys
 335 340 345

gga agt gga acc act tca ggt act acc cgt ctt cta tct ggg cac acg 1287
 Gly Ser Gly Thr Thr Ser Gly Thr Thr Arg Leu Leu Ser Gly His Thr
 350 355 360

B1
 cur f

tgt ttc acg ttg aca ggt ttg ctt ggg acg cta gta acc atg ggc ttg 1335
 Cys Phe Thr Leu Thr Gly Leu Leu Gly Thr Leu Val Thr Met Gly Leu
 365 370 375

ctg act tag ccaaagaaga gttaagaaga aaatacacac aagtatacag 1384
 Leu Thr
 380

actgttccta gtttcttaga cttatctgca tattggataa aataaatgca attgtgctct 1444

tcatttagga tgctttcatt gtctttaaga tgtgtagga atgtcaaca 1493

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 <213> Homo sapiens

<400> 6
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<210> 7
 <211> 19
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
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<210> 8
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<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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21

<210> 9
<211> 21
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<223> Description of Artificial Sequence: Primer

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21

<210> 10
<211> 29
<212> DNA
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<223> Description of Artificial Sequence: Primer

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B1
wt

<210> 11
<211> 30
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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<210> 12
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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19

<210> 13
<211> 19
<212> DNA
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<223> Description of Artificial Sequence: Primer

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19

Bl
uf